**IN THE CLAIMS**

1-19. (canceled)

20. (original) A library of nucleic acid sequences consisting essentially of nucleic acid sequences having at least about 80% protein sequence identity to a nucleic acid sequence selected from the group consisting of the *Staphylococcus aureus* open reading frames(ORFs) listed in Table1, wherein said library of nucleic acid sequences is employed to identify essential genes in *Staphylococcus*.

21. (original) A map of at least about 500-1500 transposon insertions in the genome of *Staphylococcus aureus*, wherein said map is useful for identifying genes that are essential for survival of said *Staphylococcus aureus*.

22-37. (canceled)

38. (original) The nucleic acid library of claim 20, wherein said map is in electronic form.

39. (currently amended) The library of claim ~~39~~ 38, wherein said electronic form is selected from the group consisting of magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; hybrids of these categories such as magnetic/optical storage media; computer readable forms such as a word processing text file, database format, searchable files, executable files and search program software.

40. (original) The transposon insertion map of claim 21, wherein said map is in electronic form.

41. (original) The map of claim 38, wherein said electronic form is selected from the group consisting of magnetic storage media, such as a floppy disc, a hard disc storage medium,

and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; hybrids of these categories such as magnetic/optical storage media; computer readable forms such as a word processing text file, database format, searchable files, executable files and search program software.

42. (original) A method for identifying a library of putative essential or important genes using a High Throughput Transposon Insertion Database (HTTIM), comprising:

a) mutagenizing a Staphylococcus genome with a transposon such that individual cells containing at least on transposon insertion are isolated;

b) collecting and mapping said at least one transposon insertion in each individual cell so as to form a database of transposon insertion sites, or an HTTIM;

c) comparing said database of transposon insertion sites with a database comprising the genomic sequence of the bacterium to identify open reading frames in said genomic sequence database that are not disrupted by a transposon insertion ; and

d) forming a library from said putative essential or important genes that are not disrupted by a transposon.

43. (original) The method of claim 42, wherein said bacteria is *S. aureus*.

44. (original) The method of claim 42, wherein said transposon inserts randomly into the target genome.

45. (original) The method of claim 42, wherein said transposon is 3,000 to 6,000.

46. (original) The method of claim 42, wherein said HTTIM comprises at least about 4,000 to 5,000 transposon insertion sites.

47. (original) The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 500 to 1850 genes.

48. (original) The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 1000 to 1400 genes.

49. (original) The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 600-625 genes.

50. (original) The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 530-543 genes.

51. (original) The method of claim 42, further comprising a statistical calculation for identifying putative essential or important genes.

52. (Currently amended) The method of claim 51, further comprising the statistical method applied herein.

53. (original) The method of claim 42, further comprising a physical mutagenesis experiment in order to verify essential or important genes.

54. (original) The method of claim 53, wherein said physical mutagenesis comprises knocking out a putative essential or important gene or creating a promoter swap mutant.

55. (original) An essential or important gene identified by the method of claim 53.

56. (original) An antibacterial agent that targets the gene of claim 55, or the gene product encoded by said gene.

57. (canceled)